

Figure 1

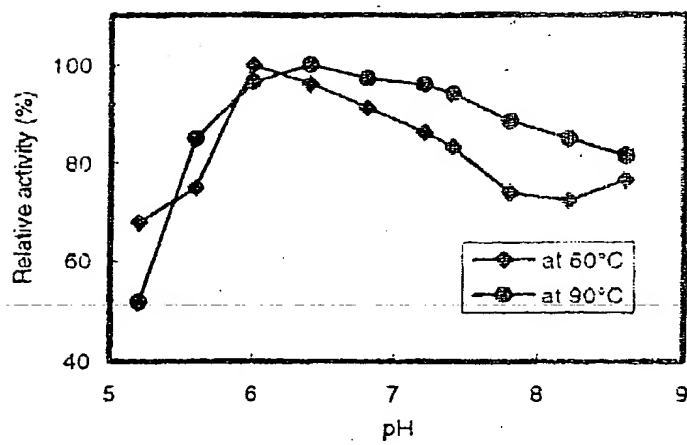
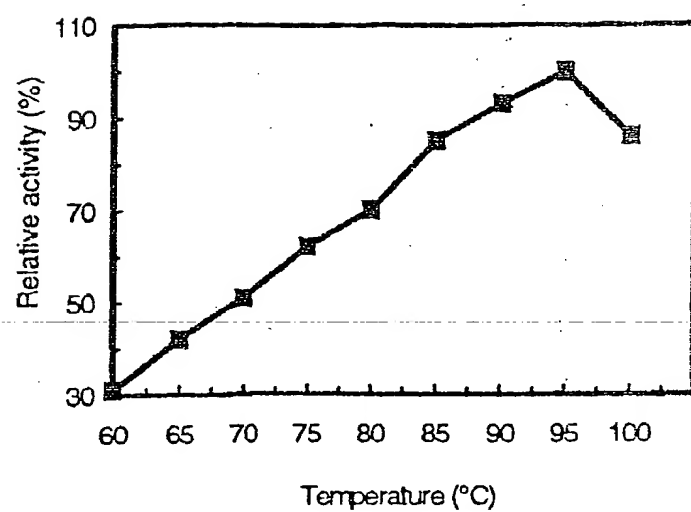
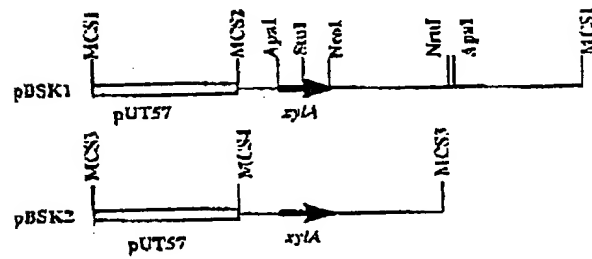
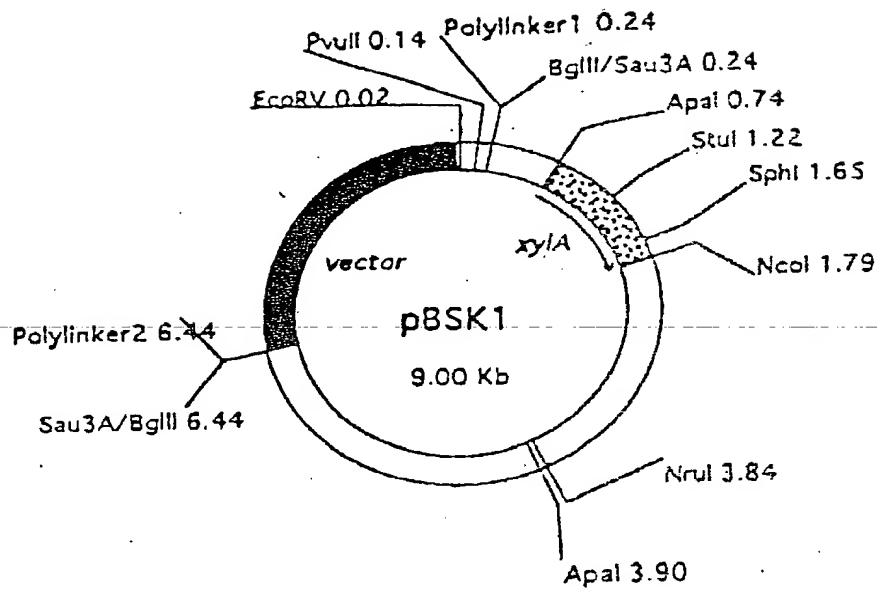


Figure 2



009280" 8 F E E E E E E

Figure 3



669200" 21222222

CACGAGCGCC TTGGTGACATGGGTGGACGAGTCACACAGGACAGGAGCGGACCGTGGCTGGACATCGGC TC TCCCTTATTTCCCGGCTCAGGGG	100
CTCTGACCTGCGGCTTCACGGTA TGCCGGGCC TG TGGGCCCCGGGTGCGGACCGCGCGCGCGCGGTTCCTGCTTCGCGTTCCTTC CAGGGACGCGC	200
TVGGCATACTAATTGTAAATCGCCCTGACGAAATAGTCGCAAGCGAGCAAGGAGCGCGGATGCACTACCGCGCCACCGCGAGGACAGGTTACCTT	300
M N Y Q P T P E D R F T F	13
CGCCCTGTGGACCGTTCGCTGGCGAGCGGCGCGGACCCCTTCGGGCGACCGGACGCGCTTCGCGCTGACGCGGCTGCGCTGCGAGCGGCTGGCGG	400
G L W T V G W Q C R D P F G D A T R P A L D P V D V Q R L A E L G	46
GGCTACGGAGTGACCTTCCACGAGCAGCAGCTGATTCCTCTCGGGGCGTTCGACACCGAGCGCGGAGGCGCACGCTCAAGCGGTTCCGCTCAGGCGCTGACG	500
A Y G V T F H D D D L I P F G A S D T E R E A H V K R F R Q A L D	79
CGACCGGCATGACCGTTCCGATGGCGACCAACCACTCTTTCACCCACCCCGCTCTTCAGGAGGGGCTTTCACGCGCAACGACCCCGCAGTGGCGCGTTA	600
A T G H T V P H A T T H L F T H P V P K A G A F T A N D R A V R R Y	113
CGCCCTGGCCAAAGACCATTCGGAACATGATCTCGCGGTCGAGCTGGCGCCCAAGGTCACGTCGCGCTCGGGCGCGCGGAGGCGCGGAGTCCGGTGCC	700
A L R K T I R N I D L A V E L G A K V Y V A W G G R E G A E S G A	146
GCCAAGGACGTGCGTGCGGCGCTGGACCCCATGAAGGAGGCTTCGACCTGCTCGCGGAGTACGTCACCTCGCAGGGCTACGACATCCGGTTTCGCCATCG	800
A K D V R A A L D R H K E A F D L L G E Y V T S Q C Y D I R F A I	179
AGCCCAAGCCGAACGAGCGCGCGCGGACATCTCGTGCCACCATCGGCCACCGCGCTCGCGTTTCATGAGCGCGCTCGAGCGCGCGGAGCTGTACGGTGT	900
E P K P N E P R G D I L L P T I G H A L A F I E R L E K P E L Y G V	213
CAACCCCGAGGTGGGCGCAGGACAGATGGCGGCTGAACTTCGCGCACGGCATCGCGAGGCTCTGTGGGCGGCGAAGCTCTTCACATGACCTCAAC	1000
N P E V G G H E Q M A G L N F P H G I A Q A L W A G K L F H I D L N	246
GGCCAGTCCGGCATCAAGTACGACCAAGGACCTGGCGCTTCGGCGCGCGGTGACCTGCGCGCGCGCTTCTGCGTGGTTCGACCTGCTCGAGAGCGCGCGCTGGG	1100
G Q S G I K Y D Q D L R F G A G D L R A A P H L V D L L E S A G W	289
AGGGTCCGCGCCACTTCGACTCAAGCCCCCGCGGACCGAGGACATCGACCGCGTGTGGGCTTCGCGCGCGCGGTGCATGCGCAACTACCTGATCCTGAA	1200
E G P R H F D P K P P R T E D I D G V W A S A A G C M R N Y L I L K	313
CGAGCGCGCGCGCGCTTCGCTGCGGACCGCGGAGGTCCAGGAGGCGCTCGCTGCGCGCGCGCTGACCGAGCTCGCGGAGCCACCGCGGCGCAGCGGCTG	1300
E R A A A A F R A D P E V Q E A L R A R L D Q L A E P T A A D G L	346
CAGGCGCTGCTGGGCGACCGCGCGCTACGAGGACTTCGACGTGGACCGCGCGCGCGCGCGGATGCGCTTCGAGCGGCTCGACCACTCGCCATGGACC	1400
Q A L L A D R T A Y E D F D V D A A A R C M A F E R L D Q L A H D	379
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H L L G A R G ***	386
GGCCCCATCGTGTCTCGCTCTCCCGGGCGCGGTGTGGGCGCGCTGC	1546

[illegible]

[illegible]

C	XYLA-STRSK	99-A ₁₀₀ -G-A ₁₀₂ -FTANDR-A ₁₀₉ -VRR- 113 112
C	XYLA-STROL	99-D ₁₀₀ -G-G ₁₀₂ -FTANDR-D ₁₀₉ -VRR- 113 112
C	XYLA-STRVO	99-D ₁₀₀ -G-G ₁₀₂ -FTANDR-D ₁₀₉ -VRR- 113 112
C	XYLA-ACTMI	99-D ₁₀₀ -G-G ₁₀₂ -FTSNDR-S ₁₀₉ -VRR- 113 112
C	XYLA-AMPSP	99-D ₁₀₀ -G-G ₁₀₂ -FTSNDR-S ₁₀₉ -VRR- 113 112
C	XYLA-THETH	99-D ₁₀₀ -G-A ₁₀₂ -FTSPDP-W ₁₀₉ -VRA- 111 112